

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 23:16:46 ; Search time 20871 Seconds
(without alignments)
11663.984 Million cell updates/sec

Title: US-10-032-256A-1
Perfect score: 5024
Sequence: 1 gcaggaggagccagggcagc.....aaaaaaaaaaaaaaaaaaaaa 5024

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	5024	100.0	5024	10	AF167987	AF167987 Mus muscu	
2	4821.6	96.0	5026	10	AF055919	AF055919 Mus muscu	

c	3	3299.8	65.7	149947	10	AC133505	AC133505	Mus muscu
	4	2142	42.6	2142	6	AX754694	AX754694	Sequence
	5	2138.8	42.6	2142	6	AX754695	AX754695	Sequence
	6	1861.8	37.1	247180	2	AC108663	AC108663	Rattus no
	7	1750	34.8	7385	9	HSA271722	AJ271722	Homo sapi
	8	1714.6	34.1	2145	6	AX056395	AX056395	Sequence
	9	1394.8	27.8	1923	6	CQ731710	CQ731710	Sequence
c	10	869	17.3	193142	2	AC113861	AC113861	Rattus no
	11	847.6	16.9	274928	2	AC114717	AC114717	Rattus no
	12	769	15.3	2931	5	BC084068	BC084068	Xenopus l
	13	765.8	15.2	2931	5	AY318877	AY318877	Xenopus l
	14	704.4	14.0	2499	5	AY318878	AY318878	Xenopus l
	15	522.2	10.4	181254	9	AL954201	AL954201	Pan trogl
	16	522.2	10.4	197872	9	AL954202	AL954202	Pan trogl
	17	510.6	10.2	63402	9	AP000260	AP000260	Homo sapi
	18	510.6	10.2	100000	9	AP000099	AP000099	Homo sapi
	19	510.6	10.2	100000	9	AP000175	AP000175	Homo sapi
c	20	510.6	10.2	144857	9	AP000036	AP000036	Homo sapi
	21	510.6	10.2	340000	9	AP001712	AP001712	Homo sapi
	22	482.2	9.6	656	6	CQ054560	CQ054560	Sequence
	23	482.2	9.6	656	6	CQ055015	CQ055015	Sequence
	24	482.2	9.6	656	6	CQ055055	CQ055055	Sequence
	25	482.2	9.6	656	6	CQ073803	CQ073803	Sequence
	26	482.2	9.6	656	6	CQ074272	CQ074272	Sequence
	27	482.2	9.6	656	6	CQ074313	CQ074313	Sequence
	28	482.2	9.6	656	6	CQ104692	CQ104692	Sequence
	29	482.2	9.6	656	6	CQ105166	CQ105166	Sequence
	30	482.2	9.6	656	6	CQ105207	CQ105207	Sequence
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	40	482.2	9.6	656	6	CQ226598	CQ226598	Sequence
	41	482.2	9.6	656	6	CQ227065	CQ227065	Sequence
	42	482.2	9.6	656	6	CQ227106	CQ227106	Sequence
	43	482.2	9.6	656	6	CQ264740	CQ264740	Sequence
	44	482.2	9.6	656	6	CQ265212	CQ265212	Sequence
	45	482.2	9.6	656	6	CQ265253	CQ265253	Sequence

ALIGNMENTS

RESULT 1
 AF167987
 LOCUS AF167987 5024 bp mRNA linear ROD 23-FEB-2000
 DEFINITION Mus musculus hormonally upregulated neu tumor-associated kinase (Hunk) mRNA, complete cds.
 ACCESSION AF167987
 VERSION AF167987.1 GI:7021318

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 5024)

AUTHORS Gardner,H.P., Wertheim,G.B., Ha,S.I., Copeland,N.G., Gilbert,D.J.,
Jenkins,N.A., Marquis,S.T. and Chodosh,L.A.

TITLE Cloning and characterization of Hunk, a novel mammalian
SNF1-related protein kinase

JOURNAL Genomics 63 (1), 46-59 (2000)

MEDLINE 20130113

PUBMED 10662544

REFERENCE 2 (bases 1 to 5024)

AUTHORS Gardner,H.P., Wertheim,G.B.W., Ha,S.I., Copeland,N.G.,
Gilbert,D.J., Jenkins,N.A., Marquis,S.T. and Chodosh,L.A.

TITLE Direct Submission

JOURNAL Submitted (11-JUL-1999) Molecular and Cellular Engineering,
University of Pennsylvania, 612 BRBII, 421 Curie Blvd.,
Philadelphia, PA 19104-6160, USA

FEATURES Location/Qualifiers

source 1. .5024
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB"
/db_xref="taxon:10090"
/chromosome="16"
/map="linked to App, Tiam1 and Erg"
/dev_stage="day 14 embryo"

gene 1. .5024
/gene="Hunk"

CDS 72. .2216
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/note="serine/threonine protein kinase"
/codon_start=1
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/protein_id="AAF35282.1"
/db_xref="GI:7021319"

/translation="MPAAAGDGLLGEPAPGGDGAEDTTRPAAACEGSFLPAWVSGV
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AEARRYIRQLISAVEHLHRAGVVHRDLKIENLLLEDNNIKLIDFGLSNCAGILGYSD
PFSTQCGSPAYAAPELLARKKYGPKIDVWSIGVNMAMLTGTLPTVEPFSRLRQYQK
MVDKAMNPLPTQLSTGAVNFLRSLLEPDVVKRPNIQQALANRWLNENYTGKVPNCVNTY
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SDIQDSICYKTQLYQIEKCRATKEPYEASLDTWTRDFEFHAVQDKPKKEQEKRGDFLH

RPF SKKLDKNLPSHKQPSPSLITQLQSTKALLKDRKASKSGFPDKDSFVCRNLFKRKTS
 DSN CVASSSMEFIPVPPRTPRIVKKLEPHQPGPGSASILPKEEPLLLDMVRSFESVD
 REDHIELLSPSHHYRILSSPVSLARRNSSERTLSQGLLSGSTSPLQTPHSTLVSAFH
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 polyA_signal 4980. .4985
 /gene="Hunk"
 ORIGIN

Query Match 100.0%; Score 5024; DB 10; Length 5024;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5024; Conservative 0; Mismatches 0; Indels 0; Gaps
 0;

Qy	1	GCAGGAGGAGCCAGGGCAGCCCCGGGAGCCGGAGGAGGAGCGGCTGCGAGCGCGGGAGCC	60
Db	1	GCAGGAGGAGCCAGGGCAGCCCCGGGAGCCGGAGGAGGAGCGGCTGCGAGCGCGGGAGCC	60
Qy	61	GAGCGAGCGCGATGCCGGCAGCGGCGGGGACGGGCTCTTGGGCGAGCCGGCGGCACCGG	120
Db	61	GAGCGAGCGCGATGCCGGCAGCGGCGGGGACGGGCTCTTGGGCGAGCCGGCGGCACCGG	120
Qy	121	GGGGCGATGGAGGCGCGGAGGACACGACCAGGCCGGCGGGCCTGCGAGGGAAGTTTCC	180
Db	121	GGGGCGATGGAGGCGCGGAGGACACGACCAGGCCGGCGGGCCTGCGAGGGAAGTTTCC	180
Qy	181	TGCCCCGCTGGGTGAGCGGCGTGTCCCGCGAGCGGCTCCGGGACTTCCAGCACCACAAGC	240
Db	181	TGCCCCGCTGGGTGAGCGGCGTGTCCCGCGAGCGGCTCCGGGACTTCCAGCACCACAAGC	240
Qy	241	GCGTGGGCAACTACCTCATCGGCAGCAGGAAGCTGGGAGAGGGCTCCTTCGCCAAGGTGC	300
Db	241	GCGTGGGCAACTACCTCATCGGCAGCAGGAAGCTGGGAGAGGGCTCCTTCGCCAAGGTGC	300
Qy	301	GCGAGGGGCTGCACGTGCTGACGGGAGAAAAGGTAGCTATCAAGGTCATCGATAAGAAAA	360
Db	301	GCGAGGGGCTGCACGTGCTGACGGGAGAAAAGGTAGCTATCAAGGTCATCGATAAGAAAA	360
Qy	361	GAGCCAAGAAAGACACCTACGTACCAAAAACCTGCGTCGAGAGGGGCAGATCCAGCAGA	420
Db	361	GAGCCAAGAAAGACACCTACGTACCAAAAACCTGCGTCGAGAGGGGCAGATCCAGCAGA	420
Qy	421	TGATCCGACACCCCAACATCACACAGCTCCTGGACATCTTGGAGACAGAGAACAGCTACT	480
Db	421	TGATCCGACACCCCAACATCACACAGCTCCTGGACATCTTGGAGACAGAGAACAGCTACT	480
Qy	481	ACCTGGTCATGGAGCTGTGTCTGGTGGCAACCTCATGCACAAGATCTACGAAAAGAAAC	540
Db	481	ACCTGGTCATGGAGCTGTGTCTGGTGGCAACCTCATGCACAAGATCTACGAAAAGAAAC	540
Qy	541	GGTTGGATGAAGCCGAGGCCCGCAGATACATCCGGCAACTCATCTCTGCGGTGGAACACC	600
Db	541	GGTTGGATGAAGCCGAGGCCCGCAGATACATCCGGCAACTCATCTCTGCGGTGGAACACC	600

Qy	601	TGCACCGTGCGGGGGTGGTTCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAG	660
Db	601	TGCACCGTGCGGGGGTGGTTCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAG	660
Qy	661	ACAATAATATCAAGCTGATTGACTTTGGCTTGAGCAACTGTGCAGGGATCCTAGGTTACT	720
Db	661	ACAATAATATCAAGCTGATTGACTTTGGCTTGAGCAACTGTGCAGGGATCCTAGGTTACT	720
Qy	721	CGGATCCATTCAGCACACAGTGTGGCAGCCCTGCCTATGCTGCGCCAGAACTGCTTGCCA	780
Db	721	CGGATCCATTCAGCACACAGTGTGGCAGCCCTGCCTATGCTGCGCCAGAACTGCTTGCCA	780
Qy	781	GGAAGAAATATGGCCCCAAAATTGATGTCTGGTCAATAGGCGTGAACATGTATGCCATGC	840
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Qy	841	TGACGGGGACCCTACCTTTCAGTGTGGAGCCTTTCAGCCTGAGGGCTCTGTATCAGAAGA	900
Db	841	TGACGGGGACCCTACCTTTCAGTGTGGAGCCTTTCAGCCTGAGGGCTCTGTATCAGAAGA	900
Qy	901	TGGTGGACAAAGCAATGAATCCCCTGCCGACCCAGCTCTCCACAGGGGCCGTCAACTTTC	960
Db	901	TGGTGGACAAAGCAATGAATCCCCTGCCGACCCAGCTCTCCACAGGGGCCGTCAACTTTC	960
Qy	961	TGCGCTCCCTCCTGGAACCAGACCCTGTGAAGAGGCCGAATATCCAGCAAGCGCTGGCGA	
1020			
Db	961	TGCGCTCCCTCCTGGAACCAGACCCTGTGAAGAGGCCGAATATCCAGCAAGCGCTGGCGA	
1020			
Qy	1021	ATCGCTGGTTGAATGAGAATTACACTGGAAAGGTGCCCTGCAATGTCACCTATCCCAACA	
1080			
Db	1021	ATCGCTGGTTGAATGAGAATTACACTGGAAAGGTGCCCTGCAATGTCACCTATCCCAACA	
1080			
Qy	1081	GGATTTCTTTGGAAGACCTGAGTCCCAGCGTGGTGCTGCACATGACTGAAAAGCTGGGCT	
1140			
Db	1081	GGATTTCTTTGGAAGACCTGAGTCCCAGCGTGGTGCTGCACATGACTGAAAAGCTGGGCT	
1140			
Qy	1141	ATAAGAACAGTGACGTCATCAACACGGTGCTCTCCAACCGCGCTGCCACATCCTGGCCA	
1200			
Db	1141	ATAAGAACAGTGACGTCATCAACACGGTGCTCTCCAACCGCGCTGCCACATCCTGGCCA	
1200			
Qy	1201	TCTACTTCCTGTTGAACAAGAACTTGAGCGCTATTTGTCAGGGAAATCAGATATCCAAG	
1260			
Db	1201	TCTACTTCCTGTTGAACAAGAACTTGAGCGCTATTTGTCAGGGAAATCAGATATCCAAG	
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Qy	1261	ATAGCATCTGCTACAAGACCCAGCTCTACCAGATAGAGAAGTGCAGAGCCACCAAGGAGC	

1320		
Db	1261	ATAGCATCTGCTACAAGACCCAGCTCTACCAGATAGAGAAGTGCAGAGCCACCAAGGAGC
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Qy	1321	CCTATGAGGCCTCCCTGGATACCTGGACGAGGGACTTTGAATTCCATGCTGTGCAGGATA
1380		
Db	1321	CCTATGAGGCCTCCCTGGATACCTGGACGAGGGACTTTGAATTCCATGCTGTGCAGGATA
1380		
Qy	1381	AAAAGCCCAAAGAACAAGAAAAAGAGGTGATTTTCTCCACCGTCCGTTTTCCAAGAAGT
1440		
Db	1381	AAAAGCCCAAAGAACAAGAAAAAGAGGTGATTTTCTCCACCGTCCGTTTTCCAAGAAGT
1440		
Qy	1441	TGGACAAGAACCTGCCTTCTCACAACAGCCATCGCCCTCGCTGATCACACAGCTCCAGA
1500		
Db	1441	TGGACAAGAACCTGCCTTCTCACAACAGCCATCGCCCTCGCTGATCACACAGCTCCAGA
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Qy	1501	GTACCAAAGCCCTGCTCAAAGACAGGAAGGCCTCCAAGTCAGGCTTCCCCGACAAAGATT
1560		
Db	1501	GTACCAAAGCCCTGCTCAAAGACAGGAAGGCCTCCAAGTCAGGCTTCCCCGACAAAGATT
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Qy	1561	CCTTCGTCTGCCGCAATCTTTTCCGAAAAACCTCTGATTCCAATTGTGTGGCTTCTTCTT
1620		
Db	1561	CCTTCGTCTGCCGCAATCTTTTCCGAAAAACCTCTGATTCCAATTGTGTGGCTTCTTCTT
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Qy	1621	CCATGGAATTCATCCCTGTCCCACCTCCCAGGACACCAAGGATTGTAAAGAACTAGAGC
1680		
Db	1621	CCATGGAATTCATCCCTGTCCCACCTCCCAGGACACCAAGGATTGTAAAGAACTAGAGC
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Qy	1681	CACACCAACCAGGGCCGGGAAGTGCCAGCATCCTCCCCAAGGAAGAGCCCCTGCTGCTGG
1740		
Db	1681	CACACCAACCAGGGCCGGGAAGTGCCAGCATCCTCCCCAAGGAAGAGCCCCTGCTGCTGG
1740		
Qy	1741	ATATGGTACGCTCCTTTGAGTCTGTGGATCGAGAGGACCACATAGAACTGCTGTCCCCTT
1800		
Db	1741	ATATGGTACGCTCCTTTGAGTCTGTGGATCGAGAGGACCACATAGAACTGCTGTCCCCTT
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Qy	1801	CTCACCATTATAGGATCCTGAGCTCGCCTGTGAGCCTGGCTCGTAGGAATTCTAGTGAGA
1860		

Db 1860	1801 CTCACCATTATAGGATCCTGAGCTCGCCTGTGAGCCTGGCTCGTAGGAATTCTAGTGAGA
Qy 1920	1861 GGAACTCTCCCAGGGGCTGCTGTCCGGAAGTACCTCACCTCTCCAACTCCACTGCATT
Db 1920	1861 GGAACTCTCCCAGGGGCTGCTGTCCGGAAGTACCTCACCTCTCCAACTCCACTGCATT
Qy 1980	1921 CCACGCTGGTCTCTTTTGCCACGAAGAAAAGAACAGCCCCCGAAAGAGGAGGGTGTGT
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Qy 2040	1981 GTTCACCGCCTCCCGTTCCAGTAATGGCCTCCTGCAGCCTCTGGGGAGCCCCAACTGTG
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Qy 2100	2041 TGAAGAGCAGGGGACGGTTCCCATGATGGGCATCGGACAGATGCTGAGGAAGCGGCACC
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Qy 2160	2101 AGAGCCTGCAGCCTTCCTCAGAGAGGTCCCTGGACGCCAGCATGTCCCCTCTGCAGCCCA
Db 2160	2101 AGAGCCTGCAGCCTTCCTCAGAGAGGTCCCTGGACGCCAGCATGTCCCCTCTGCAGCCCA
Qy 2220	2161 TAGCCCCCTCCAGCCTCTCCTTTGACATGGCCGACGGTGTCAAGGGCCAGTGTTAACCTG
Db 2220	2161 TAGCCCCCTCCAGCCTCTCCTTTGACATGGCCGACGGTGTCAAGGGCCAGTGTTAACCTG
Qy 2280	2221 GGATGGCAAGATTCTGGGTCTCTGTGAGGACAGCCACGGAACAGAGCTCCACACAGGCAG
Db 2280	2221 GGATGGCAAGATTCTGGGTCTCTGTGAGGACAGCCACGGAACAGAGCTCCACACAGGCAG
Qy 2340	2281 GCACCAGGGCATGGGTGAACAACCTCACGGGAGCATCCTTTATTCTTTTATACCTGCCAC
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Qy 2400	2341 ACAAAGTCCCACGCTTGTATCAGCTGAAGTCCACACTCAAAGTCCACGCACTTACTTAGG
Db 2400	2341 ACAAAGTCCCACGCTTGTATCAGCTGAAGTCCACACTCAAAGTCCACGCACTTACTTAGG

Qy 2460	2401	GACCCCTCTGAGACGCTGCCACTAGGGGGAGGGGGAGGGGGCAGACTGTGGGAATCACACC
Db 2460	2401	GACCCCTCTGAGACGCTGCCACTAGGGGGAGGGGGAGGGGGCAGACTGTGGGAATCACACC
Qy 2520	2461	TTCCAGCCTGAGATTTTCTTTGCTATCACCAATCACTGAGCCCTCTCCAGGATCCCCTCA
Db 2520	2461	TTCCAGCCTGAGATTTTCTTTGCTATCACCAATCACTGAGCCCTCTCCAGGATCCCCTCA
Qy 2580	2521	GTGGGCTCAGAGCTAAAAACCACACCTCCATCTGCTGGGCCAATCAGATTTCCAGACTGG
Db 2580	2521	GTGGGCTCAGAGCTAAAAACCACACCTCCATCTGCTGGGCCAATCAGATTTCCAGACTGG
Qy 2640	2581	TACCAGGTTGTCCCTCCCCTCCTCTCTGTGTGTCTCTCACAGTTCTGTAAGTACCGTCA
Db 2640	2581	TACCAGGTTGTCCCTCCCCTCCTCTCTGTGTGTCTCTCACAGTTCTGTAAGTACCGTCA
Qy 2700	2641	GTGGTCAGTTACAGTCTCACGCGGACGTGCCACTCGCTGGTAAGGACGTTACCCAACCT
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Qy 2760	2701	AGGGATCCCTCTACAGAGGGAAGCAACCTCCTTTCCCTAACAGTGAGTCCCCACAGAGT
Db 2760	2701	AGGGATCCCTCTACAGAGGGAAGCAACCTCCTTTCCCTAACAGTGAGTCCCCACAGAGT
Qy 2820	2761	GCTGAGTCACAGTGCTGGACCGGGAGGAAGATGGGATGGCGCCTCAGACAGAGATGGAAC
Db 2820	2761	GCTGAGTCACAGTGCTGGACCGGGAGGAAGATGGGATGGCGCCTCAGACAGAGATGGAAC
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Qy 2940	2881	TGACAGATTTTCTTTCTCTCTTTCTTTTCCCCTGACCTTTTCTTCTTTTGGGTTGA
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Qy	2941	AACTTGCTGAGGATTGAACGAACCTGTCCAAAGAGATCTTTCTTTATATGAAGTCATTAA

3000		
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Qy	3181	ACGTGTTTTTGTCTGAGAGGCTGCAGCTCAGATGGCCAAAAGCTGGCAACAGGAG
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Qy	3421	GTTAGAACTTAGCTGTTCTGCTGGGAGCTAGGAGCAGGCTTGCCGCCCCCTGGGAACACG
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3540		

Db 3540	3481	CTCACAAGACGGTTCGTCCCCAAAGGAAACAGTGCCCCCAAACAGGCTTTCAGTCCACT
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Db 3600	3541	 CTGTAATCTGCACCTTCCCCTCCAGGATTGAACCAAAGATGCATTTCCGGTTTTGTGACT
Qy 3660	3601	GTGCCACTCTGTGTGTCTCTTGTGGAACCTGGTGTGTCTGATCCTGTCCGGCTGGCGCT
Db 3660	3601	 GTGCCACTCTGTGTGTCTCTTGTGGAACCTGGTGTGTCTGATCCTGTCCGGCTGGCGCT
Qy 3720	3661	GGATGGAGGACTGTCTCTGTGTGCATCGTGGGCCCTGGTACTTAGCAGAGGACAAAGGGT
Db 3720	3661	 GGATGGAGGACTGTCTCTGTGTGCATCGTGGGCCCTGGTACTTAGCAGAGGACAAAGGGT
Qy 3780	3721	ACTGTTGTCAGGAGGGGAAGACTTGGCACGGGCTGGACCACAGTTAGTTTAGAAGTTATG
Db 3780	3721	 ACTGTTGTCAGGAGGGGAAGACTTGGCACGGGCTGGACCACAGTTAGTTTAGAAGTTATG
Qy 3840	3781	GAACAGCTCAGAATCTTCTGGTCTTTGACTATTTTCAGATGGGGTCAGAGACCAGAGCTGT
Db 3840	3781	 GAACAGCTCAGAATCTTCTGGTCTTTGACTATTTTCAGATGGGGTCAGAGACCAGAGCTGT
Qy 3900	3841	AGCCAGGAAGCCAGGTTTCATCATCTTGGTCCATCGATTCTAAAGTGGGCAAATTTCTGTG
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Db 3960	3901	 ACGTCACAAAGCCGGCCTTTGCCAGTGAGGGCTGAGACACAGTACAACCTGCCTCTCATTT
Qy 4020	3961	ACTGGTGGCAGGCGGCTTCCTTTGGCCTCTCAGAGCTCTGACTGAACTAGAAGAGAACAC
Db 4020	3961	 ACTGGTGGCAGGCGGCTTCCTTTGGCCTCTCAGAGCTCTGACTGAACTAGAAGAGAACAC
Qy 4080	4021	GGATTTGGCTGACCCTGGAAGAAAGCTGCTCTAGTCCTGGCTGAATTTGGTAAGACCTGG
Db 4080	4021	 GGATTTGGCTGACCCTGGAAGAAAGCTGCTCTAGTCCTGGCTGAATTTGGTAAGACCTGG

Qy 4140	4081	ACTACTTAAACCTTAGGGAGGGACTGACTCCCTCCCGAGGACCCATTACAGGAGGAGGCC
Db 4140	4081	ACTACTTAAACCTTAGGGAGGGACTGACTCCCTCCCGAGGACCCATTACAGGAGGAGGCC
Qy 4200	4141	AGGCTTTTCTCCCAGAGCTGATGGTGTTCATTTCAGCATGGCTTCCGTTTCAGTCCCA
Db 4200	4141	AGGCTTTTCTCCCAGAGCTGATGGTGTTCATTTCAGCATGGCTTCCGTTTCAGTCCCA
Qy 4260	4201	GGACTTGACACTGAAAATAGAACTCTTTAAGCAGAGAGAAGAGGAGAACCATCCACAGAC
Db 4260	4201	GGACTTGACACTGAAAATAGAACTCTTTAAGCAGAGAGAAGAGGAGAACCATCCACAGAC
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RESULT 2

AF055919

LOCUS AF055919 5026 bp mRNA linear ROD 28-APR-1999

DEFINITION Mus musculus putative serine/threonine protein kinase MAK-V (Mak-v)

mRNA, complete cds.

ACCESSION AF055919

VERSION AF055919.2 GI:4699897

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 5026)

AUTHORS Korobko, I.V., Kabishev, A.A. and Kiselev, S.L.

TITLE Identification of the new protein kinase specifically transcribed
 in mouse tumors with high metastatic potential
 JOURNAL Dokl. Akad. Nauk. 354 (4), 554-556 (1997)
 MEDLINE 97396592
 PUBMED 9273061
 REFERENCE 2 (bases 1 to 5026)
 AUTHORS Korobko, I.V.
 TITLE Direct Submission
 JOURNAL Submitted (26-MAR-1998) Laboratory of Cancer Molecular Genetics,
 Institute of Gene Biology, Russian Academy of Sciences, 34/5
 Vavilov Str., Moscow 117334, Russia
 REFERENCE 3 (bases 1 to 5026)
 AUTHORS Korobko, I.V.
 TITLE Direct Submission
 JOURNAL Submitted (28-APR-1999) Laboratory of Cancer Molecular Genetics,
 Institute of Gene Biology, Russian Academy of Sciences, 34/5
 Vavilov Str., Moscow 117334, Russia
 REMARK Sequence update by submitter
 COMMENT On Apr 28, 1999 this sequence version replaced gi:3659508.
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 Location/Qualifiers
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ORIGIN

Query Match 96.0%; Score 4821.6; DB 10; Length 5026;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 4970; Conservative 0; Mismatches 29; Indels 31; Gaps 10;

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Db 1200	1141	 ACGTCATCAACACGGTGCTCTCCAACCGCGCCTGCCACATCCTGGCCATCTACTTCCTGT	
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Db 1260	1201	 TGAACAAGAACTTGAGCGCTATTTGTCAGGGAAATCAGATATCCAAGATAGCATCTGCT	
Qy 1332	1273	ACAAGACCCAGCTCTACCAGATAGAGAAGTGCAGAGCCACCAAGGAGCCCTATGAGGCCT	

Db 1320	1261	ACAAGACCCAGCTCTACCAGATAGAGAAGTGCAGAGCCACCAAGGAGCCCTATGAGGCCT
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Db 1500	1441	 TGCCTTCTCACAAACAGCCATCGCCCTCGCTGATCACACAGCTCCAGAGTACCAAAGCCC
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Db 1800	1741	 CCTTTGAGTCTGTGGATCGAGAGGACCACATAGAACTGCTGTCCCCTTCTCACCATTATA
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Db 1920	1861	AGGGGCTGCTGTCCGGAAGTACCTCACCTCTCCAAACTCCACTGCATTCCACGCTGGTCT
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Qy 2052	1993	CCGTTCCCAGTAATGGCCTCCTGCAGCCTCTGGGGAGCCCCAACTGTGTGAAGAGCAGGG
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Qy 2292	2233	TCTGGGTCTCTGTGAGGACAGCCACGGAACAGAGCTCCACACAGGCAGGCACCAGGGCAT
Db 2280	2221	TCTGGGTCTCTGTGAGGACAGCCACGGAACAGGGCTCCACACAGGCAGGCACCAGGGCAT
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Db	4557	CTTGGACTCTGAACTCAGGTTACCCACCTGAGTCCTCAGTAGGCAGTGGACCCATTGAGA
4616		
Qy	4612	GGCAAATGAGAACAGGAGGGAGACAAGCTGTGTTCTGGGGCGCACATAAACACCTGACAG
4671		

Db 4676	4617	GGCAAATGAGAACAGGAGGGAGACAAGCTGTGTTCTGGGGCGCACATAAACACCTGACAG
Qy 4731	4672	ACGAGTCTAGGAAACCGCGTGAAAGAAGAAATGTTAAATTCCTTATTGTTTTATTATATT
Db 4736	4677	ACGAGTCTAGGAAACCGCGTGAAAGAAGAAATGTTAAATTCCTTATTGTTTTATTATATT
Qy 4791	4732	TATATGGAAAATGTGGCTATCCTTTTGTTAAGTGCAGAGTGATTGTCTGTTTGACCCAT
Db 4796	4737	TATACGGAAAATGTGGCTATCCTTTTGTTAAGTGCAGAGTGATTATCTGTTTGACCCAT
Qy 4846	4792	GA----CTGTCCTTCATGAATGAGTCTTGCCTGTGATTCTAGTC-AGCCTGTGGCTACT
Db 4856	4797	GACTGTCTGTCTTCATGAATGAGTCTTGCCTGTGATTCTAGTCAAGCCTGTGGCTACT
Qy 4906	4847	GATGGGAACGGCCGATCTGTCATCATGTGAAGTCCAGGAGGAAGAATCTATTTTAGTCAT
Db 4916	4857	GATGGGAACGGCCGATCTGTCATCATGTGAAGTCCAGGAGGAAGAGTCTATTTTAGTCAT
Qy 4965	4907	ACGA-TTTGGTCATGAGTAAGGACTATATTTATGTCACCACTATTGAATATATGTACTTT
Db 4976	4917	ACGATTTTGGTCATGAGTAAGGACTATATTTATGTCACCACTATTGAATATATGTACTTT
Qy	4966	TATAATGGCTGTGAAATACACTTTTTCCTCACAAAAAAAAAAAAAAAAAAAA 5015
Db	4977	TATAATGGCTGTGAAATACACTTTTTCCTCACAAAAAAAAAAAAAAAAAAAA 5026

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 23:13:42 ; Search time 2427 Seconds
(without alignments)
12254.133 Million cell updates/sec

Title: US-10-032-256A-1
Perfect score: 5024
Sequence: 1 gcaggaggagccagggcagc.....aaaaaaaaaaaaaaaaaaaaa 5024

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2142	42.6	2142	8	AAL60328	Aal60328 Centrosom
2	2138.8	42.6	2142	8	AAL60327	Aal60327 Centrosom
3	1750	34.8	7385	4	AAH72843	Aah72843 Human cer
4	1714.6	34.1	2145	4	AAF44660	Aaf44660 Novel pro
5	1714.6	34.1	2145	12	ADI29358	Adi29358 Human MAR
6	484.2	9.6	675	12	ACH87498	Ach87498 Human gen
7	482.2	9.6	656	4	AAI19670	Aai19670 Probe #96
8	482.2	9.6	656	4	AAI20180	Aai20180 Probe #10
9	482.2	9.6	656	4	AAI20139	Aai20139 Probe #10
10	482.2	9.6	656	4	ABA65209	Aba65209 Human foe

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11	482.2	9.6	656	4	ABA64696	Aba64696	Human	foe
12	482.2	9.6	656	4	ABA65168	Aba65168	Human	foe
13	482.2	9.6	656	4	AAI45339	Aai45339	Probe	#14
14	482.2	9.6	656	4	AAI45380	Aai45380	Probe	#14
15	482.2	9.6	656	4	AAI44865	Aai44865	Probe	#13
16	482.2	9.6	656	4	ABA46816	Aba46816	Human	bre
17	482.2	9.6	656	4	ABA47283	Aba47283	Human	bre
18	482.2	9.6	656	4	ABA47324	Aba47324	Human	bre
19	482.2	9.6	656	4	ABA31820	Aba31820	Probe	#10
20	482.2	9.6	656	4	ABA32310	Aba32310	Probe	#10
21	482.2	9.6	656	4	ABA32270	Aba32270	Probe	#10
22	482.2	9.6	656	4	AAK38862	Aak38862	Human	bon
23	482.2	9.6	656	4	AAK39367	Aak39367	Human	bon
24	482.2	9.6	656	4	AAK39326	Aak39326	Human	bon
25	482.2	9.6	656	4	AAK13626	Aak13626	Human	bra
26	482.2	9.6	656	4	AAK13586	Aak13586	Human	bra
27	482.2	9.6	656	4	AAK13131	Aak13131	Human	bra
28	482.2	9.6	656	4	ABS38447	Abs38447	Human	liv
29	482.2	9.6	656	4	ABS38914	Abs38914	Human	liv
30	482.2	9.6	656	4	ABS38955	Abs38955	Human	liv
31	482.2	9.6	656	5	AAI05884	Aai05884	Probe	#58
32	482.2	9.6	656	5	AAI05389	Aai05389	Probe	#53
33	482.2	9.6	656	5	AAI05844	Aai05844	Probe	#58
34	482.2	9.6	656	6	ABS13454	Abs13454	Human	gen
35	482.2	9.6	656	6	ABS12943	Abs12943	Human	gen
36	482.2	9.6	656	6	ABS13413	Abs13413	Human	gen
C 37	395.8	7.9	528	4	AAI22604	Aai22604	Probe	#12
C 38	395.8	7.9	528	4	ABA67679	Aba67679	Human	foe
C 39	395.8	7.9	528	4	AAI47896	Aai47896	Probe	#16
C 40	395.8	7.9	528	4	ABA49766	Aba49766	Human	bre
C 41	395.8	7.9	528	4	ABA34746	Aba34746	Probe	#13
C 42	395.8	7.9	528	4	AAK41838	Aak41838	Human	bon
C 43	395.8	7.9	528	4	AAK16096	Aak16096	Human	bra
C 44	395.8	7.9	528	4	ABS41434	Abs41434	Human	liv
C 45	395.8	7.9	528	5	AAI08280	Aai08280	Probe	#82

ALIGNMENTS

RESULT 1

AAL60328

ID AAL60328 standard; DNA; 2142 BP.

XX

AC AAL60328;

XX

DT 27-AUG-2003 (first entry)

XX

DE Centrosome-associated kinase Mak V wild-type DNA.

XX

KW Centrosome-associated kinase; cell cycle progression; therapy; enzyme;
cytostatic; Mak V; gene; ds.

XX

OS Unidentified.

XX

PN WO2003038078-A2.

XX

PD 08-MAY-2003.

XX

PF 31-OCT-2002; 2002WO-GB004940.

XX

PR 02-NOV-2001; 2001GB-00026415.

XX

XX
DR: WPI: 2003-441358/41.

XX
PS Disclosure; Page 16-17; 23pp; English.

XX
SQ Sequence 2142 BP; 532 A; 620 C; 576 G; 414 T; 0 U; 0 other;

Qy 72 ATGCCGGCAGCGGCGGGGGACGGGCTCTTGGGCGAGCCGGCGGCACCGGGGGGCGATGGA 131
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
db 1 ATGCCGGCAGCGGCGGGGGACGGGCTCTTGGGCGAGCCGGCGGCACCGGGGGGCGATGGA 60

Qy 132 GGC GCG GAG GAC AC GAC CAG GCC GCG CGC CTG CG AGG GAAG TTT CCT GCC CGC CTGG 191
pb 61 GGC GCG GAG GAC AC GAC CAG GCC GCG CGC CTG CG AGG GAAG TTT CCT GCC CGC CTGG 120

Qy 192 GTGAGCGGCGTGTCCCGCGAGCGGCTCCGGGACTTCCAGCACCACAAGCGCGTGGGCAAC 251
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 db 121 GTGAGCGGCGTGTCCCGCGAGCGGCTCCGGGACTTCCAGCACCACAAGCGCGTGGGCAAC 180

Qy 252 TACCTCATCGGCAGCAGGAAGCTGGGAGAGGGCTCCTTCGCCAAGGTGCGCGAGGGGCTG 311
db 181 TACCTCATCGGCAGCAGGAAGCTGGGAGAGGGCTCCTTCGCCAAGGTGCGCGAGGGGCTG 240

Qy 312 CACGTGCTGACGGGAGAAAAGGTAGCTATCAAGGTCATCGATAAGAAAAGAGCCAAGAAA 371
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 CACGTGCTGACGGGAGAAAAGGTAGCTATCAAGGTCATCGATAAGAAAAGAGCCAAGAAA 300

QY 372 GACACCTACGTCACCAAAAACCTGCGTCGAGAGGGGCAGATCCAGCAGATGATCCGACAC 431
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 Db 301 GACACCTACGTCACCAAAAACCTGCGTCGAGAGGGGCAGATCCAGCAGATGATCCGACAC 360

Qy 432 CCCAACATCACACAGCTCCTGGACATCTTGGAGACAGAGAACAGCTACTACCTGGTCATG 491
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 Db 361 CCCAACATCACACAGCTCCTGGACATCTTGGAGACAGAGAACAGCTACTACCTGGTCATG 420

QY 492 GAGCTGTGTCCTGGTGGCAACCTCATGCACAAGATCTACGAAAAGAAACGGTTGGATGAA 551
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 Db 421 GAGCTGTGTCCTGGTGGCAACCTCATGCACAAGATCTACGAAAAGAAACGGTTGGATGAA 480

Qy 552 GCCGAGGCCCGCAGATACATCCGGCAACTCATCTCTGCGGTGGAACACCTGCACCGTGCG 611
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db 481 GCCGAGGCCCGCAGATACATCCGGCAACTCATCTCTGCGGTGGAACACCTGCACCGTGCG 540

us-10-032-256a-1. rng

Qy	612	GGGGTGGTTCACAGAGACTTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC	671
Db	541	GGGGTGGTTCACAGAGACTTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC	600
Qy	672	AAGCTGATTGACTTTGGCTTGAGCAACTGTGCAGGGATCCTAGGTTACTCGGATCCATTC	731
Db	601	AAGCTGATTGACTTTGGCTTGAGCAACTGTGCAGGGATCCTAGGTTACTCGGATCCATTC	660
Qy	732	AGCACACAGTGTGGCAGCCCTGCCTATGCTGCGCCAGAACTGCTTGCCAGGAAGAAATAT	791
Db	661	AGCACACAGTGTGGCAGCCCTGCCTATGCTGCGCCAGAACTGCTTGCCAGGAAGAAATAT	720
Qy	792	GGCCCCAAAATTGATGTCTGGTCAATAGGCGTGAACATGTATGCCATGCTGACGGGGACC	851
Db	721	GGCCCCAAAATTGATGTCTGGTCAATAGGCGTGAACATGTATGCCATGCTGACGGGGACC	780
Qy	852	CTACCTTTCACTGTGGAGCCTTTCAGCCTGAGGGCTCTGTATCAGAAGATGGTGGACAAA	911
Db	781	CTACCTTTCACTGTGGAGCCTTTCAGCCTGAGGGCTCTGTATCAGAAGATGGTGGACAAA	840
Qy	912	GCAATGAATCCCCTGCCGACCCAGCTCTCCACAGGGGCCGTCAACTTTCTGCGCTCCCTC	971
Db	841	GCAATGAATCCCCTGCCGACCCAGCTCTCCACAGGGGCCGTCAACTTTCTGCGCTCCCTC	900
Qy	972	CTGGAACCAGACCCTGTGAAGAGGCCGAATATCCAGCAAGCGCTGGCGAATCGCTGGTTG	1031
Db	901	CTGGAACCAGACCCTGTGAAGAGGCCGAATATCCAGCAAGCGCTGGCGAATCGCTGGTTG	960
Qy	1032	AATGAGAATTACACTGGAAAGGTGCCCTGCAATGTCACCTATCCCAACAGGATTTCTTTG	1091
Db	961	AATGAGAATTACACTGGAAAGGTGCCCTGCAATGTCACCTATCCCAACAGGATTTCTTTG	1020
Qy	1092	GAAGACCTGAGTCCCAGCGTGGTGTGCACATGACTGAAAAGCTGGGCTATAAGAACAGT	1151
Db	1021	GAAGACCTGAGTCCCAGCGTGGTGTGCACATGACTGAAAAGCTGGGCTATAAGAACAGT	1080
Qy	1152	GACGTCATCAACACGGTGCTCTCCAACCGCGCTGCCACATCCTGGCCATCTACTTCCTG	1211
Db	1081	GACGTCATCAACACGGTGCTCTCCAACCGCGCTGCCACATCCTGGCCATCTACTTCCTG	1140
Qy	1212	TTGAACAAGAAACTTGAGCGCTATTTGTGAGGGAAATCAGATATCCAAGATAGCATCTGC	1271
Db	1141	TTGAACAAGAAACTTGAGCGCTATTTGTGAGGGAAATCAGATATCCAAGATAGCATCTGC	1200
Qy	1272	TACAAGACCCAGCTCTACCAGATAGAGAAGTGCAGAGCCACCAAGGAGCCCTATGAGGCC	1331
Db	1201	TACAAGACCCAGCTCTACCAGATAGAGAAGTGCAGAGCCACCAAGGAGCCCTATGAGGCC	1260
Qy	1332	TCCCTGGATACCTGGACGAGGGACTTTGAATTCCATGCTGTGCAGGATAAAAAGGCCAAA	1391
Db	1261	TCCCTGGATACCTGGACGAGGGACTTTGAATTCCATGCTGTGCAGGATAAAAAGGCCAAA	1320
Qy	1392	GAACAAGAAAAAAGAGGTGATTTTCTCCACCGTCCGTTTTCCAAGAAGTTGGACAAGAAC	1451
Db	1321	GAACAAGAAAAAAGAGGTGATTTTCTCCACCGTCCGTTTTCCAAGAAGTTGGACAAGAAC	1380
Qy	1452	CTGCCTTCTCACAAACAGCCATCGCCCTCGCTGATCACACAGCTCCAGAGTACCAAAGCC	1511
Db	1381	CTGCCTTCTCACAAACAGCCATCGCCCTCGCTGATCACACAGCTCCAGAGTACCAAAGCC	1440
Qy	1512	CTGCTCAAAGACAGGAAGGCCTCCAAGTCAGGCTTCCCCGACAAAGATTCTTCGTCTGC	1571
Db	1441	CTGCTCAAAGACAGGAAGGCCTCCAAGTCAGGCTTCCCCGACAAAGATTCTTCGTCTGC	1500

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Qy	1572	CGCAATCTTTTCCGAAAAACCTCTGATTCCAATTGTGTGGCTTCTTCTTCATGGAATTC	1631
Db	1501	CGCAATCTTTTCCGAAAAACCTCTGATTCCAATTGTGTGGCTTCTTCTTCATGGAATTC	1560
Qy	1632	ATCCCTGTCCCACCTCCCAGGACACCAAGGATTGTAAAGAACTAGAGCCACACCAACCA	1691
Db	1561	ATCCCTGTCCCACCTCCCAGGACACCAAGGATTGTAAAGAACTAGAGCCACACCAACCA	1620
Qy	1692	GGGCCGGGAAGTGCCAGCATCCTCCCAAGGAAGAGCCCCTGCTGCTGGATATGGTACGC	1751
Db	1621	GGGCCGGGAAGTGCCAGCATCCTCCCAAGGAAGAGCCCCTGCTGCTGGATATGGTACGC	1680
Qy	1752	TCCTTTGAGTCTGTGGATCGAGAGGACCACATAGAACTGCTGTCCCCTTCTCACCATTAT	1811
Db	1681	TCCTTTGAGTCTGTGGATCGAGAGGACCACATAGAACTGCTGTCCCCTTCTCACCATTAT	1740
Qy	1812	AGGATCCTGAGCTCGCCTGTGAGCCTGGCTCGTAGGAATTCTAGTGAGAGGACACTCTCC	1871
Db	1741	AGGATCCTGAGCTCGCCTGTGAGCCTGGCTCGTAGGAATTCTAGTGAGAGGACACTCTCC	1800
Qy	1872	CAGGGGCTGCTGTCCGGAAGTACCTCACCTCTCCAACTCCACTGCATTCCACGCTGGTC	1931
Db	1801	CAGGGGCTGCTGTCCGGAAGTACCTCACCTCTCCAACTCCACTGCATTCCACGCTGGTC	1860
Qy	1932	TCTTTTGCCACGAAGAAAAGAACAGCCCCCGAAAGAGGAGGGTGTGTGTTACCCGCCT	1991
Db	1861	TCTTTTGCCACGAAGAAAAGAACAGCCCCCGAAAGAGGAGGGTGTGTGTTACCCGCCT	1920
Qy	1992	CCCGTTCCCAGTAATGGCCTCCTGCAGCCTCTGGGGAGCCCCAACTGTGTGAAGAGCAGG	2051
Db	1921	CCCGTTCCCAGTAATGGCCTCCTGCAGCCTCTGGGGAGCCCCAACTGTGTGAAGAGCAGG	1980
Qy	2052	GGACGGTTCCCCATGATGGGCATCGGACAGATGCTGAGGAAGCGGCACCAGAGCCTGCAG	2111
Db	1981	GGACGGTTCCCCATGATGGGCATCGGACAGATGCTGAGGAAGCGGCACCAGAGCCTGCAG	2040
Qy	2112	CCTTCCTCAGAGAGGTCCCTGGACGCCAGCATGTCCCCTCTGCAGCCCATAGCCCCCTCC	2171
Db	2041	CCTTCCTCAGAGAGGTCCCTGGACGCCAGCATGTCCCCTCTGCAGCCCATAGCCCCCTCC	2100
Qy	2172	AGCCTCTCCTTTGACATGGCCGACGGTGTCAAGGGCCAGTGT	2213
Db	2101	AGCCTCTCCTTTGACATGGCCGACGGTGTCAAGGGCCAGTGT	2142

us-10-032-256a-1.rnpb

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2005, 05:51:28 ; Search time 2639 Seconds
(without alignments)
11549.510 Million cell updates/sec

Title: US-10-032-256A-1
Perfect score: 5024
Sequence: 1 gcaggaggagccagggcagc.....aaaaaaaaaaaaaaaaaaaaa 5024

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
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- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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				us-10-032-256a-1.rnpb		
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	3	482.2	9.6	656	9	US-09-864-761-17590
	4	482.2	9.6	656	9	US-09-864-761-17630
c	5	395.8	7.9	528	9	US-09-864-761-20066
	6	377.2	7.5	482	9	US-09-764-868-224
	7	377.2	7.5	482	11	US-09-764-875-72
	8	377.2	7.5	482	11	US-09-764-875-389
	9	377.2	7.5	482	17	US-10-242-355-186
c	10	345	6.9	474	9	US-09-864-761-3290
	11	338.8	6.7	470	9	US-09-864-761-326
	12	272.6	5.4	459	9	US-09-864-761-807
	13	272.6	5.4	459	9	US-09-864-761-849
	14	229	4.6	297	9	US-09-864-761-17591
	15	229	4.6	297	9	US-09-864-761-17631
	16	194.4	3.9	457	9	US-09-864-761-325
	17	180	3.6	502	16	US-10-029-386-6982
	18	174.8	3.5	1205	18	US-10-363-345A-19069
c	19	174.8	3.5	1205	18	US-10-363-345A-19070
	20	174.8	3.5	1205	19	US-10-363-483A-19069
c	21	174.8	3.5	1205	19	US-10-363-483A-19070
	22	174.8	3.5	56153	17	US-10-221-714A-519
	23	171.2	3.4	472	9	US-09-864-761-808
	24	171.2	3.4	472	9	US-09-864-761-850
	25	155	3.1	1975	17	US-10-424-599-3569
	26	155	3.1	1975	17	US-10-425-114-8714
	27	148.8	3.0	2110	18	US-10-739-930-5028
	28	148.6	3.0	1317	17	US-10-425-114-9772
	29	148.6	3.0	2022	17	US-10-425-114-6306
	30	148.2	2.9	2150	18	US-10-425-115-101612
c	31	146.8	2.9	466	9	US-09-864-761-426
	32	146.6	2.9	1770	17	US-10-425-114-35453
	33	145.4	2.9	474	9	US-09-864-761-10591
	34	143.8	2.9	2073	17	US-10-424-599-3567
	35	143.6	2.9	2138	17	US-10-425-114-2343
	36	143.6	2.9	2922	18	US-10-425-115-128036
	37	143.4	2.9	1933	17	US-10-425-114-3580
	38	143.4	2.9	1945	17	US-10-425-114-28167
	39	143.4	2.9	2124	18	US-10-425-115-28948
	40	143	2.8	237	9	US-09-864-761-27212
	41	143	2.8	249	9	US-09-864-761-20252
c	42	142.8	2.8	189	9	US-09-864-761-17225
	43	142.4	2.8	2044	18	US-10-425-115-154128
	44	141.8	2.8	453	9	US-09-864-761-3482
	45	141.6	2.8	1812	17	US-10-425-114-29601

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	Sequence 17590, A
	Sequence 17630, A
	Sequence 20066, A
	Sequence 224, App
	Sequence 72, App1
	Sequence 389, App
	Sequence 186, App
	Sequence 3290, Ap
	Sequence 326, App
	Sequence 807, App
	Sequence 849, App
	Sequence 17591, A
	Sequence 17631, A
	Sequence 325, App
	Sequence 6982, Ap
	Sequence 19069, A
	Sequence 19070, A
	Sequence 19069, A
	Sequence 19070, A
	Sequence 519, App
	Sequence 808, App
	Sequence 850, App
	Sequence 3569, Ap
	Sequence 8714, Ap
	Sequence 5028, Ap
	Sequence 9772, Ap
	Sequence 6306, Ap
	Sequence 101612, A
	Sequence 426, App
	Sequence 35453, A
	Sequence 10591, A
	Sequence 3567, Ap
	Sequence 2343, Ap
	Sequence 128036, A
	Sequence 3580, Ap
	Sequence 28167, A
	Sequence 28948, A
	Sequence 27212, A
	Sequence 20252, A
	Sequence 17225, A
	Sequence 154128, A
	Sequence 3482, Ap
	Sequence 29601, A

ALIGNMENTS

RESULT 1

US-10-029-386-20693

; Sequence 20693, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE

; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20693
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP001712.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: NT HIT: gi14780177, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P57058, EVALUE 1.00e-109
; OTHER INFORMATION: EST_HUMAN HIT: BF529471.1, EVALUE 0.00e+00
US-10-029-386-20693

Query Match 9.6%; Score 484.2; DB 16; Length 675;
Best Local Similarity 83.6%; Pred. No. 3.9e-127;
Matches 549; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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QY      1556 AGATTCCTTCGTCTGCCGCAATCTTTTCCGAAAAACCTCTGATTCCAATTGTGTGGCTTC 1615
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Db       18 AGATTCCTTTGGCTGCCGCAATATTTTCCGCAAAACCTCAGATTCCAATTGTGTGGCTTC 77

QY      1616 TTCTTCCATGGAATTCATCCCTGTCCCACCTCCCAGGACACCAAGGATTGTAAAGAAACT 1675
          |||
Db       78 TTCTTCCATGGAGTTCATCCCCGTGCCACCGCCAGGACCCCGAGGATTGTGAAGAAACC 137

QY      1676 AGAGCCACACCAACCAGGGCCGGGAAGTGCCAGCATCCTCCCCAAGGAAGAGCCCCTGCT 1735
          |||
Db      138 GGAGCCCCATCAGCCAGGGCCCGGAAGCACTGGCATCCCCCACAAGGAAGACCCCCTGAT 197

QY      1736 GCTGGATATGGTACGCTCCTTTGAGTCTGTGGATCGAGAGGACCACATAGAAGTGTGTGTC 1795
          |||
Db      198 GCTGGACATGGTGCCTCCTTCGAGTCTGTGGATCGCGACGACCACGTAGAAGTGTGTGTC 257

QY      1796 CCCTTCTCACCATTATAGGATCCTGAGCTCGCCTGTGAGCCTGGCTCGTAGGAATTCTAG 1855
          |||
Db      258 TCCCTCTCATCACTACAGGATTCTGAACTCCCGGTGAGCTTGGCTCGCAGAAATTCCAG 317

QY      1856 TGAGAGGACACTCTCCCAGGGGCTGCTGTCCGGAAGTACCTCACCTCTCCAAACTCCACT 1915
          |||
Db      318 CGAGAGGACGCTGTCCCCGGGTCTGCCATCCGGAAGCATGTCGCCTCTCCATACTCCTTT 377

QY      1916 GCATTCCACGCTGGTCTCTTTTGCCACGAAGAAAAGAAGAGAGGAGGG 1975
          |||
Db      378 GCATCCAACCTCTGGTCTCTTTTGCTCACGAAGATAAGAAGAGAGGAGGG 437

QY      1976 TGTGTGTTACCGCCTCCCGTTCCAGTAATGGCCTCCTGCAGCCTCTGGGGAGCCCCAA 2035
          |||
Db      438 CCTGTGTTGCCACCTCCGTTCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAA 497

QY      2036 CTGTGTGAAGAGCAGGGGACGGTTCCCATGATGGGCATCGGACAGATGCTGAGGAAGCG 2095
          |||
Db      498 TTGTGTGAAAAGCCGAGGCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCG 557

QY      2096 GCACCAGAGCCTGCAGCCTTCTCAGAGAGGTCCCTGGACGCCAGCATGTCCCCTCTGCA 2155
          |||
Db      558 CCATCAGAGTCTGCAGCCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCACTGCA 617
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us-10-032-256a-1.rnpb

Qy 2156 GCCCATAGCCCCCTCCAGCCTCTCCTTTGACATGGCCGACGGTGTCAAGGGCCAGTG 2212
||| ||||| | ||| ||||||||| ||| |||||
Db 618 GCCCCTAGCCCCCTGTGAACCTTGCCTTTGACATGGCCGATGGGGTCAAGACCCAGTG 674

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OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 23:17:42 ; Search time 14801 Seconds
(without alignments)
12920.403 Million cell updates/sec

Title: US-10-032-256A-1
Perfect score: 5024
Sequence: 1 gcaggaggagccagggcagc.....aaaaaaaaaaaaaaaaaaaaa 5024

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	785.2	15.6	791	5	BU056886	BU056886 UI-M-FO0-
2	783.4	15.6	851	6	CB845007	CB845007 M2PN-0573
3	781	15.5	852	5	BQ180567	BQ180567 UI-M-EX0-
4	779.4	15.5	864	6	CA325070	CA325070 UI-M-FY0-
5	770	15.3	771	6	CB249687	CB249687 UI-M-EX0-
6	769.4	15.3	775	6	CA316433	CA316433 UI-M-FW0-
7	759	15.1	810	6	CB518393	CB518393 UI-M-GH0-
8	753.2	15.0	805	7	CF729648	CF729648 UI-M-HD0-

9	748	14.9	760	7	CK635586	CK635586	UI-M-HN0-
10	737	14.7	768	5	BQ770004	BQ770004	UI-M-FI0-
11	732.8	14.6	736	6	CB245694	CB245694	UI-M-FY0-
12	725.2	14.4	730	7	CO432726	CO432726	UI-M-HX0-
13	723	14.4	735	6	CA328675	CA328675	UI-M-FY0-
14	721.6	14.4	809	4	BI456696	BI456696	603172171
15	714.6	14.2	746	7	CN457776	CN457776	UI-M-HN0-
16	712.4	14.2	715	7	CN531867	CN531867	UI-M-HQ0-
17	711.2	14.2	724	6	CD351138	CD351138	UI-M-FY0-
18	703.4	14.0	716	7	CN456014	CN456014	UI-M-HN0-
19	703	14.0	703	7	CF733065	CF733065	UI-M-HB0-
20	700.6	13.9	708	5	BM945579	BM945579	UI-M-EM0-
21	699.4	13.9	732	7	CO429800	CO429800	UI-M-HX0-
22	698.4	13.9	770	6	CB526563	CB526563	UI-M-FY0-
23	692.4	13.8	717	6	BY741170	BY741170	BY741170
24	684	13.6	684	5	BQ444125	BQ444125	UI-M-EX0-
25	683	13.6	862	6	CB204649	CB204649	AGENCOURT
26	681.4	13.6	684	7	CF741692	CF741692	UI-M-HB0-
27	679.4	13.5	693	5	BQ442075	BQ442075	UI-M-EX0-
28	678.8	13.5	682	7	CN694047	CN694047	E0345C04-
29	677.6	13.5	721	5	BU609323	BU609323	UI-M-FR0-
30	661	13.2	945	2	BF577874	BF577874	602092184
c 31	654.8	13.0	676	7	CO043684	CO043684	UI-M-EX0-
32	653.4	13.0	658	7	CN526322	CN526322	UI-M-HN0-
33	652.4	13.0	701	6	CB058030	CB058030	NISC_js11
34	650.6	12.9	757	6	CA511170	CA511170	UI-R-FJ0-
35	644	12.8	760	2	BF163408	BF163408	601771773
36	639.4	12.7	642	7	CF739350	CF739350	UI-M-HD0-
37	634.6	12.6	952	5	BU504020	BU504020	AGENCOURT
38	634.4	12.6	636	7	CF901214	CF901214	A0325D06-
39	625.2	12.4	630	7	CO434600	CO434600	UI-M-HX0-
40	624.8	12.4	639	7	CF734578	CF734578	UI-M-HB0-
41	624.6	12.4	688	5	BU613918	BU613918	UI-M-FR0-
42	617.4	12.3	678	7	CF734744	CF734744	UI-M-HB0-
43	614.4	12.2	616	7	CN702563	CN702563	E0463H09-
44	604	12.0	898	4	BI731620	BI731620	603353048
45	602	12.0	647	7	CN532251	CN532251	UI-M-HQ0-

ALIGNMENTS

RESULT 1

BU056886

LOCUS BU056886 791 bp mRNA linear EST 26-AUG-2002

DEFINITION UI-M-FO0-bzz-h-14-0-UI.r1 NIH_BMAP_F00 Mus musculus cDNA clone
IMAGE:6412861 5', mRNA sequence.

ACCESSION BU056886

VERSION BU056886.1 GI:22496963

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 791)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.

FEATURES Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6412861"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_F00"
 /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is TGAGAGAGCC. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 15.6%; Score 785.2; DB 5; Length 791;
 Best Local Similarity 99.5%; Pred. No. 1.3e-176;
 Matches 787; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 509 CAACCTCATGCACAAGATCTACGAAAAGAAACGGTTGGATGAAGCCGAGGCCCGCAGATA 568
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 Db 1 CAACCTCATGCACAAGATCTACGAAAAGAAACGGTTGGATGAAGCCGAGGCCCGCAGATA 60

Qy 569 CATCCGGCAACTCATCTCTGCGGTGGAACACCTGCACCGTGCAGGGGTGGTTTCACAGAGA 628
 |||
 Db 61 CATCCGGCAACTCATCTCTGCGGTGGAACACCTGCACCGTGCAGGGGTGGTTTCACAGAGA 120

Qy 629 CTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATCAAGCTGATTGACTTTGG 688
 |||
 Db 121 CTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATCAAGCTGATTGACTTTGG 180

Qy	689	CTTGAGCAACTGTGCAGGGATCCTAGGTTACTCGGATCCATTCAGCACACAGTGTGGCAG	748
Db	181	CTTGAGCAACTGTGCAGGGATCCTAGGTTACTCGGATCCATTCAGCACACAGTGTGGCAG	240
Qy	749	CCCTGCCTATGCTGCGCCAGAACTGCTTGCCAGGAAGAAATATGGCCCCAAAATTGATGT	808
Db	241	CCCTGCCTATGCTGCGCCAGAACTGCTTGCCAGGAAGAAATATGGCCCCAAAATTGATGT	300
Qy	809	CTGGTCAATAGGCGTGAACATGTATGCCATGCTGACGGGGACCCTACCTTTCACTGTGGA	868
Db	301	CTGGTCAATAGGCGTGAACATGTATGCCATGCTGACGGGGACCCTACCTTTCACTGTGGA	360
Qy	869	GCCTTTCAGCCTGAGGGCTCTGTATCAGAAAGATGGTGGACAAAGCAATGAATCCCCTGCC	928
Db	361	GCCTTTCAGCCTGAGGGCTCTGTATCAGAAAGATGGTGGACAAAGCAATGAATCCCCTGCC	420
Qy	929	GACCCAGCTCTCCACAGGGGCCGTCAACTTTCTGCGCTCCCTCCTGGAACCAGACCCTGT	988
Db	421	GACCCAGCTCTCCACAGGGGCCGTCAACTTTCTGCGCTCCCTCCTGGAACCAGACCCTGT	480
Qy	989	GAAGAGGCCGAATATCCAGCAAGCGCTGGCGAATCGCTGGTTGAATGAGAATTACACTGG	1048
Db	481	GAAGAGGCCGAATATCCAGCAAGCGCTGGCGAATCGCTGGTTGAATGAGAATTACACTGG	540
Qy	1049	AAAGGTGCCCTGCAATGTCACCTATCCCAACAGGATTTCTTTGGAAGACCTGAGTCCCAG	1108
Db	541	AAAGGTGCCCTGCAATGTCACCTATCCCAACAGGATTTCTTTGGAAGACCTGAGTNCAG	600
Qy	1109	CGTGGTGCTGCACATGACTGAAAAGCTGGGCTATAAGAACAGTGACGTCATCAACACGGT	1168
Db	601	CGTGGTGCTGCACATGACTGAAAAGCTGGGCTATAAGAACAGTGACGTCATCAACACGGT	660
Qy	1169	GCTCTCCAACCGCGCCTGCCACATCCTGGCCATCTACTTCCTGTTGAACAAGAACTTGA	1228
Db	661	GCTCTCCAACCGCGCCTGCCACATCCTGGCCATCTACTTCCTGGTTGACAAGAACTTGA	720
Qy	1229	GCGCTATTTGTCAGGGAAATCAGATATCCAAGATAGCATCTGCTACAAGACCCAGCTCTA	1288
Db	721	GCGCTATTTGTCAGGGAAATCAGATATCCAAGATAGCATCTGCTACAAGACCCAGCTCTA	780
Qy	1289	CCAGATAGAGA	1299
Db	781	CCAGATAGAGA	791

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 20, 2005, 09:58:04 ; Search time 312 Seconds
(without alignments)
12455.668 Million cell updates/sec

Title: US-10-032-256A-1
Perfect score: 9026
Sequence: 1 gcaggaggagccagggcagc.....aaaaaaaaaaaaaaaaaaaaa 5024

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10032256/runat_19042005_181218_13540/app_query.fasta_1.5
191

-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10032256_@CGN_1_1_366_@runat_19042005_181218_13540 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
1	3722	41.2	714	6	AAO29754	Aao29754	Centrosom
2	3476	38.5	714	4	AAB65633	Aab65633	Novel pro
3	3476	38.5	714	8	ADI29240	Adi29240	Human MAR
4	983	10.9	218	4	AAM13906	Aaml3906	Peptide #
5	983	10.9	218	4	AAM14403	Aaml4403	Peptide #
6	983	10.9	218	4	ABB32851	Abb32851	Peptide #
7	983	10.9	218	4	ABB33351	Abb33351	Peptide #
8	983	10.9	218	4	AAM26312	Aam26312	Peptide #
9	983	10.9	218	4	AAM26816	Aam26816	Peptide #
10	983	10.9	218	4	ABB27681	Abb27681	Human pep
11	983	10.9	218	4	ABB28176	Abb28176	Human pep
12	983	10.9	218	4	ABB18811	Abb18811	Protein #
13	983	10.9	218	4	ABB18333	Abb18333	Protein #
14	983	10.9	218	4	AAM66037	Aam66037	Human bon
15	983	10.9	218	4	AAM66530	Aam66530	Human bon
16	983	10.9	218	4	AAM53654	Aam53654	Human bra
17	983	10.9	218	4	AAM54137	Aam54137	Human bra
18	983	10.9	218	4	ABG47703	Abg47703	Human liv
19	983	10.9	218	4	ABG48198	Abg48198	Human liv
20	983	10.9	218	4	AAM01649	Aam01649	Peptide #
21	983	10.9	218	4	AAM02130	Aam02130	Peptide #
22	983	10.9	218	5	ABG36182	Abg36182	Human pep
23	983	10.9	218	5	ABG35685	Abg35685	Human pep
24	761	8.4	157	4	AAM99769	Aam99769	Human exc
25	761	8.4	157	4	AAU17272	Aau17272	Novel sig
26	761	8.4	157	4	AAU87152	Aau87152	Novel cen
27	761	8.4	157	4	AAU87469	Aau87469	Novel cen
28	761	8.4	157	4	AAM42584	Aam42584	Human kid
29	761	8.4	157	7	ADB93980	Adb93980	Human nov
30	761	8.4	157	8	ADI54784	Adi54784	Novel hum
31	761	8.4	157	8	ADI54467	Adi54467	Novel hum
32	651	7.2	744	5	AAE19049	Aae19049	Human PAR
33	651	7.2	761	6	ABP96068	Abp96068	Human pro
34	649.5	7.2	729	2	AAW37158	Aaw37158	Human Twe
35	649.5	7.2	729	4	AAB65628	Aab65628	Novel pro
36	649.5	7.2	729	6	AAE33552	Aae33552	Human mic
37	649.5	7.2	729	7	ADC34765	Adc34765	Human C-T
38	649.5	7.2	729	7	ADG91724	Adg91724	Human mic
39	649.5	7.2	729	8	ADI29234	Adi29234	Human MAR
40	649.5	7.2	729	8	ADI29438	Adi29438	Human MAR
41	646.5	7.2	795	5	AAE19052	Aae19052	Human PAR
42	646.5	7.2	795	5	AAE16258	Aae16258	Human kin
43	646.5	7.2	795	6	AAE33551	Aae33551	Human mic
44	646.5	7.2	795	7	ADG91723	Adg91723	Human mic
45	646.5	7.2	795	8	ADQ88278	Adq88278	Human 138

ALIGNMENTS

RESULT 1

AAO29754

ID AAO29754 standard; protein; 714 AA.

XX

AC AAO29754;

XX

DT 27-AUG-2003 (first entry)

XX

DE Centrosome-associated kinase Mak V (K91R) mutant protein.

XX

KW Centrosome-associated kinase; cell cycle progression; therapy; enzyme;
KW cytostatic; Mak V; gene; mutant; mutein.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 91

FT /note= "Wild-type Lys is substituted with Arg"

XX

PN WO2003038078-A2.

XX

PD 08-MAY-2003.

XX

PF 31-OCT-2002; 2002WO-GB004940.

XX

PR 02-NOV-2001; 2001GB-00026415.

XX

PA (UYWA-) UNIV WARWICK.

XX

PI Stott D, Seung-Woon S, Craig GM;

XX

DR WPI; 2003-441358/41.

DR N-PSDB; AAL60327.

XX

PT New centrosome-associated kinase with decreased or no kinase activity,
PT useful for identifying inhibitors or activators of cell cycle
PT progression, for use in manufacturing a treatment for uncontrolled cell
PT cycle progression.

XX

PS Claim 2; Page 14-16; 23pp; English.

XX

CC The invention relates to centrosome-associated kinase with decreased or
CC no kinase activity useful for identifying inhibitors or activators of
CC cell cycle progression. The invention is useful for identifying an
CC inhibitor or activator of cell cycle progression, which is useful in
CC manufacturing a medicament for treating uncontrolled cell cycle
CC progression. The present sequence is centrosome-associated kinase Mak V
CC mutant protein

XX

SQ Sequence 714 AA;

Alignment Scores:

Pred. No.:	3.29e-297	Length:	714
Score:	3722.00	Matches:	713
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.86%	Mismatches:	0
Query Match:	41.24%	Indels:	0

DB:

6

Gaps:

0

US-10-032-256A-1 (1-5024) x AAO29754 (1-714)

Qy 72 ATGCCGGCAGCGGCGGGGACGGGCTCTTGGGCGAGCCGGCGGCACCGGGGGGCGATGGA 131
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Db 1 MetProAlaAlaAlaGlyAspGlyLeuLeuGlyGluProAlaAlaProGlyGlyAspGly 20

Qy 132 GGCGCGGAGGACACGACCAGGCCGGCGGGCCCTGCGAGGGAAGTTTCCTGCCCCGCTGG 191
|||||
Db 21 GlyAlaGluAspThrThrArgProAlaAlaAlaCysGluGlySerPheLeuProAlaTrp 40

Qy 192 GTGAGCGGCGTGTCCCGCGAGCGGCTCCGGGACTTCCAGCACCACAAGCGCGTGGGCAAC 251
|||||
Db 41 ValSerGlyValSerArgGluArgLeuArgAspPheGlnHisHisLysArgValGlyAsn 60

Qy 252 TACCTCATCGGCAGCAGGAAGCTGGGAGAGGGCTCCTTCGCCAAGGTGCGCGAGGGGCTG 311
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Db 61 TyrLeuIleGlySerArgLysLeuGlyGluGlySerPheAlaLysValArgGluGlyLeu 80

Qy 312 CACGTGCTGACGGGAGAAAAGGTAGCTATCAAGGTCATCGATAAGAAAAGAGCCAAGAAA 371
|||||:::|||||
Db 81 HisValLeuThrGlyGluLysValAlaIleArgValIleAspLysLysArgAlaLysLys 100

Qy 372 GACACCTACGTCACCAAAAACCTGCGTCGAGAGGGGCAGATCCAGCAGATGATCCGACAC 431
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Db 101 AspThrTyrValThrLysAsnLeuArgArgGluGlyGlnIleGlnGlnMetIleArgHis 120

Qy 432 CCCAACATCACACAGCTCCTGGACATCTTGGAGACAGAGAACAGCTACTACCTGGTCATG 491
|||||
Db 121 ProAsnIleThrGlnLeuLeuAspIleLeuGluThrGluAsnSerTyrTyrLeuValMet 140

Qy 492 GAGCTGTGTCTCTGGTGGCAACCTCATGCACAAGATCTACGAAAAGAAACGGTTGGATGAA 551
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Db 141 GluLeuCysProGlyGlyAsnLeuMetHisLysIleTyrGluLysLysArgLeuAspGlu 160

Qy 552 GCCGAGGCCCGCAGATACATCCGGCAACTCATCTCTGCGGTGGAACACCTGCACCGTGCG 611
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Db 161 AlaGluAlaArgArgTyrIleArgGlnLeuIleSerAlaValGluHisLeuHisArgAla 180

Qy 612 GGGGTGGTTCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC 671
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Db 181 GlyValValHisArgAspLeuLysIleGluAsnLeuLeuLeuAspGluAspAsnAsnIle 200

Qy 672 AAGCTGATTGACTTTGGCTTGAGCAACTGTGCAGGGATCCTAGGTTACTCGGATCCATTC 731
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Db 201 LysLeuIleAspPheGlyLeuSerAsnCysAlaGlyIleLeuGlyTyrSerAspProPhe 220

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Qy	1092	GAAGACCTGAGTCCCAGCGTGGTGTGCACATGACTGAAAAGCTGGGCTATAAGAACAGT	1151	
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Qy	1152	GACGTCATCAACACGGTGCTCTCCAACCGCGCTGCCACATCCTGGCCATCTACTTCCTG	1211	
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Qy	1212	TTGAACAAGAACTTGAGCGCTATTTGTCAGGGAAATCAGATATCCAAGATAGCATCTGC	1271	
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	651	7.2	744	9	US-09-919-585-3	Sequence 3, Appli
8	649.5	7.2	729	14	US-10-142-356-11	Sequence 11, Appl
9	649.5	7.2	729	14	US-10-195-101-33	Sequence 33, Appl
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20	640	7.1	752	15	US-10-258-106-16	Sequence 16, Appl
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ALIGNMENTS

RESULT 1

US-09-864-761-33631

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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
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; PRIOR FILING DATE: 2001-01-30
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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4	600		6.6	774	2	I48609			probable serine/th
5	594.5		6.6	1246	2	G89287			protein H39E23.1 [
6	594		6.6	726	2	T33998			hypothetical prote
7	592		6.6	562	2	T29858			hypothetical prote
8	591.5		6.6	891	2	T40503			protein kinase kin
9	589.5		6.5	891	2	A38903			protein kinase 1 -
10	574		6.4	504	2	T10449			probable serine/th
11	573.5		6.4	798	2	JC7500			qik protein - chic
12	565		6.3	512	2	T52633			serine/threonine-s
13	564.5		6.3	651	2	S52244			p69Eg3 protein - A
14	562.5		6.2	1398	2	T13741			hypothetical prote
15	554		6.1	511	1	A56009			serine/threonine-s
16	548.5		6.1	633	1	A26030			serine/threonine-s
17	547		6.1	453	2	G86141			protein T25K16.13
18	545.5		6.0	622	1	S44859			serine/threonine-s
19	543.5		6.0	504	2	T07415			probable serine/th
20	543.5		6.0	512	1	JC1446			serine/threonine-s
21	543		6.0	552	1	A53621			[hydroxymethylglut
22	542		6.0	552	1	S51025			[hydroxymethylglut
23	541		6.0	480	2	A86427			probable serine/th
24	540.5		6.0	576	2	T41587			probable carbon ca
25	535		5.9	672	2	T50259			probable serine/th
26	533.5		5.9	602	2	S72513			FOG2 protein - yea
27	533		5.9	1147	2	S64930			serine/threonine-s
28	531.5		5.9	445	2	T50802			serine/threonine p
29	531		5.9	510	2	T04145			serine/threonine p
30	529		5.9	445	2	T09903			serine/threonine-s
31	527.5		5.8	441	2	C84667			probable protein k
32	525		5.8	473	1	S59941			serine/threonine-s
33	525		5.8	481	2	I49072			protein kinase - m
34	525		5.8	512	2	T07788			probable serine/th
35	517.5		5.7	440	2	T14735			probable serine/th
36	515.5		5.7	513	1	S60303			serine/threonine-s
37	514.5		5.7	489	2	T04862			probable serine/th
38	513		5.7	887	2	T20941			hypothetical prote
39	510.5		5.7	421	2	T48202			protein kinase AK2
40	510.5		5.7	421	2	E96522			hypothetical prote
41	509.5		5.6	502	1	A41361			serine/threonine-s
42	508.5		5.6	440	2	T14736			probable serine/th
43	508		5.6	746	2	S62365			SNF1-related prote
44	505.5		5.6	472	2	B90100			SNF-related kinase
45	503		5.6	469	2	B84644			probable protein k

ALIGNMENTS

RESULT 1

G01025

serine/threonine protein kinase - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C;Accession: G01025
R;Navarro, E.
submitted to the EMBL Data Library, April 1996
A;Reference number: H00564
A;Accession: G01025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-745 <NAV>
A;Cross-references: UNIPROT:Q15524; UNIPROT:Q96HB3; EMBL:X97630; NID:g1310674
C;Superfamily: protein kinase homology
F;18-271/Domain: protein kinase homology <KIN>

Pred. No.:	1.57e-19	Length:	745
Score:	640.00	Matches:	195
Percent Similarity:	46.21%	Conservative:	122
Best Local Similarity:	28.43%	Mismatches:	225
Query Match:	7.09%	Indels:	144
DB:	2	Gaps:	28

Qy	222	GACTTCAGACACCACAAGCGCGTGGGCAACTACCTCATCGGCAGCAGGAAGCTGGGAGAG	281
		:: :::: :: :::	
Db	12	AspGluGlnProHis-----IleGlyAsnTyrArgLeu---LeuLysThrIleGlyLys	28
Qy	282	GGCTCCTTCGCCAAGGTGCGCGAGGGGCTGCACGTGCTGACGGGAGAAAAGGTAGCTATC	341
		:: ::: :: ::: :::	
Db	29	GlyAsnPheAlaLysValLysLeuAlaArgHisIleLeuThrGlyLysGluValAlaVal	48
Qy	342	AAGGTCATCGATAAGAAAAGAGCCAAGAAAGACACCTACGTCACCAAACCTGCGTCGA	401
		:: :::: :: :: ::	
Db	49	LysIleIleAspLysThrGlnLeuAsnSerSerSer-----LeuGlnLysLeuPheArg	66
Qy	402	GAGGGGCAGATCCAGCAGATGATCCGACACCCCAACATCACACAGCTCCTGGACATCTTG	461
		::: ::::::: :: :::::::	
Db	67	GluValArgIleMetLysValLeuAsnHisProAsnIleValLysLeuPheGluValIle	86
Qy	462	GAGACAGAGAACAGCTACTACCTGGTCATGGAGCTGTGTCCTGGTGGAACCTCATGCAC	521
		:: :::	
Db	87	GluThrGluLysThrLeuTyrLeuValMetGluTyrAlaSerGlyGlyGluValPheAsp	106
Qy	522	AAGATCTACGAAAAGAAACGGTTGGATGAAGCCGAGGCCCGCAGATACATCCGGCAACTC	581
		::: ::: :::	
Db	107	TyrLeuValAlaHisGlyArgMetLysGluLysGluAlaArgAlaLysPheArgGlnIle	126
Qy	582	ATCTCTGCGGTGGAACACCTGCACCGTGCGGGGGTGGTTTCACAGAGACTTGAAGATAGAG	641
		::: ::: ::: ::	
Db	127	ValSerAlaValGlnTyrCysHisGlnLysPheIleValHisArgAspLeuLysAlaGlu	146
Qy	642	AATTGCTACTAGATGAAGACAATAATATCAAGCTGATTGACTTTGGCTTGAGCAACTGT	701
		::	
Db	147	AsnLeuLeuLeuAspAlaAspMetAsnIleLysIleAlaAspPheGlyPheSerAsn---	165
Qy	702	GCAGGGATCCTAGGTTACTCGGATCCATTACGACACAGTGTGGCAGCCCTGCCTATGCT	761
		: : : : :	

Db 166 -----GluPheThrPheGlyAsnLysLeuAspThrPheCysGlySerProProTyrAla 183
 Qy 762 GCGCCAGAACTGCTTGCCAGGAAGAAATAT---GGCCCCAAAATTGATGTCTGGTCAATA 818
 ||||| ||||| |||||:|||||:|
 Db 184 AlaProGluLeuPheGlnGlyLysLysTyrAspGlyProGluValAspValTrpSerLeu 203
 Qy 819 GCGGTGAACATGTATGCCATGCTGACGGGGACCCTACCTTTCACCTGTGGAGCCTTTCAGC 878
 ||||| :||| :|||:|||||:| :||| :|||
 Db 204 GlyValIleLeuTyrThrLeuValSerGlySerLeuProPheAspGlyGln-----Asn 221
 Qy 879 CTGAGGGCTCTGTATCAGAAGATGGTGGACAAAGCAATGAATCCCCTGCCGACCCAGCTC 938
 |||:| ||| :|||:| :||| :||| :||| :|||
 Db 222 LeuLysGluLeuArgGluArgValLeu---ArgGlyLysTyrArgIleProPheTyrMet 240
 Qy 939 TCCACAGGGGCCGTCAACTTTCTGCGCTCCCTCCTGGAACCAGACCCTGTGAAGAGGCCG 998
 ||||| ||| |||:| ||| :||| |||||
 Db 241 SerThrAspCysGluAsnLeuLeuLysLysPheLeuIleLeuAsnProSerLysArgGly 260
 Qy 999 AATATCCAGCAAGCGCTGGCGAATCGCTGGTTGAATGAGAATTACACTGGAAAGGTGCCC 1058
 :|||:| ||| :|||:| ||| :||| :||| :|||
 Db 261 ThrLeuGluGlnIleMetLysAspArgTrpMetAsnValGlyHisGluAsp----- 277
 Qy 1059 TGCAATGTCACCTATCCCAACAGGATTTCTTTGGAAGACCTGAGTCCCAGCGTGGTG--- 1115
 :|||:| ||| |||
 Db 278 -----AspGluLeuLysProTyrValGluPro 286
 Qy 1116 -----CTGCACATGACTGAAAAGCTGGGCTATAAGAAC 1148
 :||| :|||:| |||
 Db 287 LeuProAspTyrLysAspProArgArgThrGluLeuMetValSerMetGlyTyrThrArg 306
 Qy 1149 AGTGACGTCATCAACACGGTGCTCTCCAACCGCGCCTGCCACATCCTGGCCATCTACTTC 1208
 :|||:| :|||:| ||| :|||:| |||
 Db 307 GluGluIleGlnAspSerLeuValGlyGlnArgTyrAsnGluValMetAlaThrTyrLeu 326
 Qy 1209 CTGTTGAACAAGAACTTGAGCGCTATTTGTGAGGGAAATCAGATATCCAA---GATAGC 1265
 ||||| ||| |||:|||:| |||:|
 Db 327 LeuLeuGlyTyrLys-----SerSerGluLeuGluGlyAspThr 339
 Qy 1266 ATCTGCTACAAGACCCAGCTCTACCAGATAGAGAAGTGCAGAGCCACCAAGGAGCCCTAT 1325
 ||| ||| :|||
 Db 340 IleThrLeuLysProArg-----Pro 346
 Qy 1326 GAGGCCTCCCTGGATACCTGGACGAGGGACTTTGAATTCATGCTGTGCAG----- 1376
 ||| ||| :||| ||| ||| |||||
 Db 347 SerAlaAspLeuThrAsnSerSerAlaGlnPheProSerHisLysValGlnArgSerVal 366
 Qy 1377 GATAAAAAGCCCAAGAACAA-----GAAAAAGAGGTGATTTTCTC-----CAC 1421
 |||||:||| :|||:| ||| :|||
 Db 367 SerAlaAsnProLysGlnArgArgPheSerAspGlnAlaGlyProAlaIleProThrSer 386
 Qy 1422 CGTCCGTTTTTCCAAGAAGTTGGACAAGAACCTGCCTTCTCACAACAGCCATCGCCCTCG 1481
 :|||:| ||| :|||:| |||
 Db 387 AsnSerTyrSerLysLysThrGlnSerAsnAsnAlaGluAsnLysArgProGlu----- 404
 Qy 1482 CTGATCACACAGCTCCAGAGTACCAAAGCCCTGCTCAAAGACAGGAAGGCCTCCAAGTCA 1541
 :|||:| ||| :|||
 Db 405 -----GluAspArgGluSerGlyArgLys 412

Qy 1542 GGCTTCCCCGACAAAGATTCCTTCGTCTGCCGCAATCTTTTCCGAAAAACCTCTGATTCC 1601

Db 412 ----- 412

Qy 1602 AATTGTGTGGCTTCTTCTTCCATGGAATTCATCCCTGTCCCACCTCCCAGGACACCAAGG 1661
 |||||::: ::| ||||| |||

Db 413 -----AlaSerSerThrAlaLys-----ValProAlaSerProLeuProGly 426

Qy 1662 ATTGTAAAGAACTAGAGCCACACCAACCAGGGCCGGGAAGTGCCAGCATCCTC----- 1715
 ::: ::||| ||| ||| ::: ||:::|

Db 427 LeuGluArgLys-----LysThrThrProThrProSerThrAsnSerValLeuSerThr 444

Qy 1716 -----CCCAAGGAAGAGCCCCTGCTGCTGGATATGGTACGCTCCTTTGAGTCT 1763
 ::: ||||| |||

Db 445 SerThrAsnArgSerArgAsnSerProLeuLeuGluArgAlaSerLeuGlyGlnAlaSer 464

Qy 1764 GTGGATCGA---GAGGACCACATAGAAGTGTGTCCCCTTCTCACCATTATAGGATCCTG 1820
 ::: ::||| ::: ::

Db 465 IleGlnAsnGlyLysAspSerLeuThrMetProGlySerArgAlaSerThrAlaSerAla 484

Qy 1821 AGCTCGCCTGTGAGCCTGGCTCGTAGGAATTCTAGTGAGAGGACACTCTCCCAGGGGCTG 1880
 ||::: ||||| ||||| :::::

Db 485 SerAlaGlyValSerAlaAlaArgProArgGlnHisGlnLysSer----- 499

Qy 1881 CTGTCCGGAAGTACCTCACCTCTCCAACTCCACTGCATTCCACGCTGGTCTCTTTTGCC 1940
 ::||| |||

Db 500 MetSerGlySerValHisPro----- 506

Qy 1941 CACGAAGAAAAGAACAGCCCCCGAAAGAGGAGGGTGTGTGTTACCGCCTCCCGTTCCC 2000
 ::::: ||||| ||| ||| |||

Db 507 AsnLysAlaSerGlyLeuProProThrGluSerAsn---CysGluValProArgProSer 525

Qy 2001 AGTAATGGCCTCCTGCAGCCTCTGGGGAGCCCCAACTGT-----GTGAAGAGCAGGGGA 2054
 ::: ||::: |||||::: ::: ||| |||

Db 526 ThrAlaProGlnArgValProValAlaSerProSerAlaHisAsnIleSerSerSerGly 545

Qy 2055 CGGTTCCCATGATGGGCATCGGACAGATGCTGAGGAAGCGGCACCAGAGCCTGCAGCCT 2114
 ||:::| ||| |||||::: ::: |

Db 546 -GlyAlaPro-Asp-----ArgThrAsnPheProArgGlyValSerSerArgSerThrP 563

Qy 2115 TC-----CTCAGAGAGGTCCCTGGACGCCAGCATGTCCCCTCTGCAGCCCATA 2162
 || |||||:::| ||:::|:::|

Db 563 heHisAlaGlyGlnLeuArgGlnValArgAspGlnGlnAsnLeuProTyrGlyVal---T 582

Qy 2163 GCCCCCTCCAGCCT 2176
 ::||| |||

Db 582 hrProAlaSerPro 586

us-10-032-256a-1.n2p.rup

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 20, 2005, 10:10:28 ; Search time 394 Seconds
(without alignments)
13059.319 Million cell updates/sec

Title: US-10-032-256A-1
Perfect score: 9026
Sequence: 1 gcaggaggagccagggcagc.....aaaaaaaaaaaaaaaaaaaaa 5024

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10032256/runat_19042005_181219_13547/app_query.fasta_1.5191

-DB=UniProt_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10032256_@CGN_1_1_477_@runat_19042005_181219_13547 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3720	41.2	714	1	HUNK_MOUSE	088866 mus musculu
2	3482	38.6	714	2	Q68UT7	Q68ut7 pan troglod
3	3476	38.5	714	1	HUNK_HUMAN	P57058 homo sapien
4	2222.5	24.6	691	2	Q6VZ18	Q6vz18 xenopus lae
5	2004	22.2	626	2	Q6VZ17	Q6vz17 xenopus lae

us-10-032-256a-1.n2p.rup						
6	1284	14.2	279	2	Q68UT6	Q68ut6 pan troglod
7	691	7.7	792	2	Q6INT7	Q6int7 xenopus lae
8	648	7.2	771	2	Q69ZI7	Q69zi7 mus musculu
9	646.5	7.2	795	2	Q9P0L2	Q9p0l2 homo sapien
10	646	7.2	752	2	Q8CIP4	Q8cip4 mus musculu
11	644.5	7.1	793	2	O08678	O08678 rattus norv
12	640	7.1	752	1	MRK4_HUMAN	Q96l34 homo sapien
13	638	7.1	745	2	Q15524	Q15524 homo sapien
14	636	7.0	797	2	Q8VHF0	Q8vhf0 rattus norv
15	634	7.0	729	2	Q9JKE4	Q9jke4 mus musculu
16	633	7.0	744	2	Q9JKE5	Q9jke5 mus musculu
17	632	7.0	752	2	Q8NG37	Q8ng37 homo sapien
18	632	7.0	795	2	Q8VHJ5	Q8vhj5 mus musculu
19	631	7.0	888	2	Q8BR95	Q8br95 mus musculu
20	629	7.0	778	2	Q96HB3	Q96hb3 homo sapien
21	628.5	7.0	755	2	Q7KZI7	Q7kzi7 homo sapien
22	628	7.0	722	2	Q6PDR4	Q6pdr4 mus musculu
23	628	7.0	780	2	Q804T1	Q804t1 xenopus lae
24	627	6.9	776	1	MRK3_HUMAN	P27448 homo sapien
25	625.5	6.9	942	2	Q8MVW9	Q8mvw9 haemonchus
26	625.5	6.9	1066	2	Q8MVX0	Q8mvx0 haemonchus
27	623	6.9	722	2	O08679	O08679 rattus norv
28	621.5	6.9	691	2	Q96RG0	Q96rg0 homo sapien
29	620	6.9	776	2	Q7ZYL7	Q7zy17 xenopus lae
30	620	6.9	785	2	Q8QGV3	Q8qgv3 xenopus lae
31	619.5	6.9	1371	2	Q9Y2K2	Q9y2k2 homo sapien
32	618.5	6.9	719	2	Q68A18	Q68a18 homo sapien
33	618.5	6.9	993	2	Q7KRK4	Q7krk4 drosophila
34	617.5	6.8	1098	2	Q7KRK7	Q7krk7 drosophila
35	614.5	6.8	722	2	Q802W0	Q802w0 brachydanio
36	608	6.7	966	2	Q8MVX2	Q8mvx2 haemonchus
37	607	6.7	725	2	Q804T2	Q804t2 xenopus lae
38	606.5	6.7	834	2	Q8MVX1	Q8mvx1 haemonchus
39	606	6.7	1096	2	Q17368	Q17368 caenorhabdi
40	602	6.7	1189	2	Q6PHV1	Q6phv1 brachydanio
41	601.5	6.7	1192	2	Q17346	Q17346 caenorhabdi
42	601.5	6.7	1192	2	Q9TW45	Q9tw45 caenorhabdi
43	600	6.6	774	1	MRK2_MOUSE	Q05512 mus musculu
44	598.5	6.6	462	2	O75271	O75271 homo sapien
45	598	6.6	1187	2	Q6NSM8	Q6nsm8 brachydanio

ALIGNMENTS

RESULT 1

HUNK_MOUSE

ID HUNK_MOUSE STANDARD; PRT; 714 AA.
AC O88866;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hormonally up-regulated neu tumor-associated kinase (EC 2.7.1.37)
DE (Serine/threonine-protein kinase MAK-V).
GN Name=Hunk; Synonyms=Makv;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/SN; TISSUE=Mammary gland;
RX MEDLINE=97396592; PubMed=9273061;
RA Korobko I.V., Kabishev A.A., Kiselev S.L.;

us-10-032-256a-1.n2p.rup

RT "Identification of the new protein kinase specifically transcribed in
RT mouse tumors with high metastatic potential.";
RL Dokl. Akad. Nauk SSSR 354:554-556(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB; TISSUE=Mammary gland;
RX MEDLINE=20130113; PubMed=10662544; DOI=10.1006/geno.1999.6078;
RA Gardner H.P., Wertheim G.B.W., Ha S.I., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Marquis S.T., Chodosh L.A.;
RT "Cloning and characterization of Hunk, a novel mammalian SNF1-related
RT protein kinase.";
RL Genomics 63:46-59(2000).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. SNF1
CC subfamily.

CC -----
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DR EMBL; AF055919; AAC61489.1; -.
DR EMBL; AF167987; AAF35282.1; -.
DR HSSP; Q63450; 1A06.
DR MGD; MGI:1347352; Hunk.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 62 320 Protein kinase.
FT NP_BIND 68 76 ATP (By similarity).
FT BINDING 91 91 ATP (By similarity).
FT ACT_SITE 186 186 Proton acceptor (By similarity).
FT CONFLICT 697 697 T -> I (in Ref. 2).
SQ SEQUENCE 714 AA; 79602 MW; D35A53E7A8D9BD1F CRC64;

Alignment Scores:

Pred. No.:	2.42e-206	Length:	714
Score:	3720.00	Matches:	713
Percent Similarity:	99.86%	Conservative:	0
Best Local Similarity:	99.86%	Mismatches:	1
Query Match:	41.21%	Indels:	0
DB:	1	Gaps:	0

US-10-032-256A-1 (1-5024) x HUNK_MOUSE (1-714)

Qy	72	ATGCCGGCAGCGGCGGGGACGGGCTCTTGGGCGAGCCGGCGGCACCGGGGGGCGATGGA	131
db	1	MetProAlaAlaAlaGlyAspGlyLeuLeuGlyGluProAlaAlaProGlyGlyAspGly	20
Qy	132	GGCGCGGAGGACACGACCAGGCCGGCGGGCCTGCGAGGGAAGTTTCCTGCCCGCCTGG	191
db	21	GlyAlaGluAspThrThrArgProAlaAlaAlaCysGluGlySerPheLeuProAlaTrp	40

Qy 192 GTGAGCGGCGTGTCCCGCGAGCGGCTCCGGGACTTCCAGCACCACAAGCGCGTGGGCAAC 251
 Db 41 ValSerGlyValSerArgGluArgLeuArgAspPheGlnHisHisLysArgValGlyAsn 60
 Qy 252 TACCTCATCGGCAGCAGGAAGCTGGGAGAGGGCTCCTTCGCCAAGGTGCGCGAGGGGCTG 311
 Db 61 TyrLeuIleGlySerArgLysLeuGlyGluGlySerPheAlaLysValArgGluGlyLeu 80
 Qy 312 CACGTGCTGACGGGAGAAAAGGTAGCTATCAAGGTATCGATAAGAAAAGAGCCAAGAAA 371
 Db 81 HisValLeuThrGlyGluLysValAlaIleLysValIleAspLysLysArgAlaLysLys 100
 Qy 372 GACACCTACGTACCAAAAACCTGCGTCGAGAGGGGCAGATCCAGCAGATGATCCGACAC 431
 Db 101 AspThrTyrValThrLysAsnLeuArgArgGluGlyGlnIleGlnGlnMetIleArgHis 120
 Qy 432 CCCAACATCACACAGCTCCTGGACATCTTGGAGACAGAGAACAGCTACTACCTGGTCATG 491
 Db 121 ProAsnIleThrGlnLeuLeuAspIleLeuGluThrGluAsnSerTyrTyrLeuValMet 140
 Qy 492 GAGCTGTGTCTGGTGGCAACCTCATGCACAAGATCTACGAAAAGAAACGGTTGGATGAA 551
 Db 141 GluLeucysProGlyGlyAsnLeuMethisLysIleTyrGluLysLysArgLeuAspGlu 160
 Qy 552 GCCGAGGCCCGCAGATACATCCGGCAACTCATCTCTGCGGTGGAACACCTGCACCGTGCG 611
 Db 161 AlaGluAlaArgArgTyrIleArgGlnLeuIleSerAlaValGluHisLeuHisArgAla 180
 Qy 612 GGGGTGGTTCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC 671
 Db 181 GlyValValHisArgAspLeuLysIleGluAsnLeuLeuLeuAspGluAspAsnAsnIle 200
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; Sequence 14904, Application US/09621976
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; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
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13	1508	30.0	7257	115	US-60-452-680-11294	Sequence 11294, A
14	1506.4	30.0	7257	49	US-10-170-235-32765	Sequence 32765, A
15	1040.2	20.7	1343	48	US-10-144-771-20325	Sequence 20325, A
16	1040.2	20.7	1343	106	US-60-360-207-20325	Sequence 20325, A
c 17	766.8	15.3	996	87	US-60-184-774-251	Sequence 251, App
18	733	14.6	1872	23	US-09-523-654A-31	Sequence 31, Appl
19	733	14.6	1872	23	US-09-523-654B-31	Sequence 31, Appl
20	733	14.6	1872	39	US-09-902-919-31	Sequence 31, Appl

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22	510.8	10.2	142692	120	US-60-500-337-19459	Sequence 19459, A
c 23	510.6	10.2	1748349	41	US-09-947-914-48	Sequence 48, Appl
24	487	9.7	546	44	US-09-963-353-207	Sequence 207, App
25	487	9.7	546	53	US-10-375-682-207	Sequence 207, App
26	484.2	9.6	675	46	US-10-029-386-20693	Sequence 20693, A
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31	482.2	9.6	656	37	US-09-864-761-17590	Sequence 17590, A
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36	482.2	9.6	656	49	US-10-182-995-10286	Sequence 10286, A
37	482.2	9.6	656	49	US-10-182-995-10736	Sequence 10736, A
38	482.2	9.6	656	49	US-10-182-995-10776	Sequence 10776, A
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40	482.2	9.6	656	49	US-10-182-997-10072	Sequence 10072, A
41	482.2	9.6	656	49	US-10-182-997-10113	Sequence 10113, A
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ALIGNMENTS

RESULT 1

US-10-032-256A-1

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; Sequence 1, Application US/10032256A
; GENERAL INFORMATION:
; APPLICANT: CHODOSH, Lewis A
; APPLICANT: GARDNER, Heather P
; TITLE OF INVENTION: HORMONALLY UP-REGULATED, NEU-TUMOR-ASSOCIATED KINASE
; FILE REFERENCE: 22253-70421
; CURRENT APPLICATION NUMBER: US/10/032,256A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: 60/257,073
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5024
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US-10-032-256A-1
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8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
9: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq2:*
11: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq3:*
12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	171.2	3.4	472	10	US-11-060-756-1385	Sequence 1385, Ap
2	171.2	3.4	472	10	US-11-060-756-5657	Sequence 5657, Ap
3	155	3.1	1975	2	PCT-US04-42316-17	Sequence 17, Appl
4	148.8	3.0	2110	2	PCT-US04-42316-25	Sequence 25, Appl
5	148.6	3.0	2022	2	PCT-US04-42316-15	Sequence 15, Appl
6	142.4	2.8	1993	2	PCT-US04-42316-9	Sequence 9, Appli
7	142.4	2.8	2023	2	PCT-US04-42316-13	Sequence 13, Appl
8	141.6	2.8	1885	2	PCT-US04-42316-19	Sequence 19, Appl
9	140	2.8	1838	2	PCT-US04-42316-23	Sequence 23, Appl
10	138.6	2.8	600	10	US-11-060-756-1783	Sequence 1783, Ap
11	138.6	2.8	600	10	US-11-060-756-1784	Sequence 1784, Ap

				us-10-032-256a-1.rnpn		
12	138.6	2.8	600	10	US-11-060-756-6055	Sequence 6055, Ap
13	138.6	2.8	600	10	US-11-060-756-6056	Sequence 6056, Ap
14	131	2.6	1766	2	PCT-US04-42316-50	Sequence 50, Appl
15	130.8	2.6	3226	12	US-60-660-590-61	Sequence 61, Appl
16	130.8	2.6	4917	7	US-10-204-639-87	Sequence 87, Appl
17	129.4	2.6	1563	2	PCT-US04-42316-1	Sequence 1, Appli
18	129.2	2.6	3609	12	US-60-660-590-62	Sequence 62, Appl
19	127.4	2.5	4723	12	US-60-646-841-19	Sequence 19, Appl
20	124.4	2.5	1235	2	PCT-US04-42316-32	Sequence 32, Appl
21	122.8	2.4	2524	2	PCT-US04-42316-3	Sequence 3, Appli
22	122.8	2.4	2530	2	PCT-US04-42316-5	Sequence 5, Appli
23	121.2	2.4	2083	2	PCT-US04-42316-40	Sequence 40, Appl
24	120.6	2.4	2959	2	PCT-US04-42360-2300	Sequence 2300, Ap
25	119.6	2.4	1700	2	PCT-US04-42316-7	Sequence 7, Appli
26	119.2	2.4	1840	2	PCT-US04-42316-36	Sequence 36, Appl
27	118.2	2.4	2986	7	US-10-524-979-1	Sequence 1, Appli
28	113.2	2.3	756	7	US-10-524-979-5	Sequence 5, Appli
29	111.8	2.2	2449	2	PCT-US04-42316-42	Sequence 42, Appl
30	109.8	2.2	2470	2	PCT-US03-27894-21	Sequence 21, Appl
31	109.8	2.2	2501	7	US-10-955-054A-138	Sequence 138, App
32	109.6	2.2	1124	2	PCT-US04-42316-38	Sequence 38, Appl
33	103	2.1	1788	2	PCT-US04-42316-44	Sequence 44, Appl
34	102	2.0	3010	2	PCT-US04-23309-57	Sequence 57, Appl
35	100.8	2.0	1400	10	US-11-060-756-720	Sequence 720, App
36	100.8	2.0	1400	10	US-11-060-756-4992	Sequence 4992, Ap
37	99.8	2.0	2729	2	PCT-US04-23309-36	Sequence 36, Appl
38	98.8	2.0	4836	2	PCT-US04-23309-16	Sequence 16, Appl
c 39	98.4	2.0	13361	7	US-10-472-963-1665	Sequence 1665, Ap
40	98.2	2.0	1400	10	US-11-060-756-3835	Sequence 3835, Ap
41	98.2	2.0	1400	10	US-11-060-756-8107	Sequence 8107, Ap
42	98.2	2.0	3437	7	US-10-488-292-1	Sequence 1, Appli
43	96.6	1.9	1104	7	US-10-259-740A-1	Sequence 1, Appli
44	96.6	1.9	9862	7	US-10-259-740A-3	Sequence 3, Appli
45	95.2	1.9	1402	10	US-11-059-535-2112	Sequence 2112, Ap

ALIGNMENTS

RESULT 1

US-11-060-756-1385

; Sequence 1385, Application US/11060756

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William Martin

; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

; TITLE OF INVENTION: Target Genes

; FILE REFERENCE: AM101083 (031896-042000)

; CURRENT APPLICATION NUMBER: US/11/060,756

; CURRENT FILING DATE: 2005-02-18

; NUMBER OF SEQ ID NOS: 303284

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1385

; LENGTH: 472

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-060-756-1385

Query Match 3.4%; Score 171.2; DB 10; Length 472;
 Best Local Similarity 87.0%; Pred. No. 4.3e-21;
 Matches 188; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

[illegible]